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* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 16:08:21 ON 01 NOV 2002

=> file registry
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'REGISTRY' ENTERED AT 16:09:02 ON 01 NOV 2002
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Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 31 OCT 2002 HIGHEST RN 468711-89-9
DICTIONARY FILE UPDATES: 31 OCT 2002 HIGHEST RN 468711-89-9

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

Please note that search-term pricing does apply when conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> s gargarggnacngcngtncc/sqsn
L1 61 GARGARGGNACNGCNGTNCC/SQSN

=> s garttycaraargayathgaymg/sqsn
L2 6 GARTTYCARAARGAYATHGAYMG/SQSN

=> s ttygtnaaygtnathtgyggngc/sqsn
L3 3 TTYGTNAAYGTNATHTGYGGNGC/SQSN

=> que tgnckdatnswytcrtcraaytc/sqsn
L4 QUE TGNCKDATNSWYTCRTCRAAYTC/SQSN

=> que tgnckrtcyttrtangcrtcytg/sqsn
L5 QUE TGNCKRTCYTTRTANGCRTCYTG/SQSN

=> que ggngcraadatnckytgnckrtc/sqsn
L6 QUE GGNGCRAADATNCKYTGNCKRTC/SQSN

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```
=> s l4
L7            3 TGNCKDATNSWYTCRTCRAAYTC/SQSN

=> s l5
L8            3 TGNCKRTCYTTRTANGCRTCYTG/SQSN

=> s l65
L65 NOT FOUND
The L-number entered has not been defined in this session, or it
has been deleted.  To see the L-numbers currently defined in this
session, enter DISPLAY HISTORY at an arrow prompt (=>).

=> s l6
L9            3 GGNGCRAADATNCKYTGNCKRTC/SQSN

=> FIL BIOSIS MEDLINE CAPLUS EMBASE
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                   189.78     189.99

FILE 'BIOSIS' ENTERED AT 16:57:44 ON 01 NOV 2002
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FILE 'MEDLINE' ENTERED AT 16:57:44 ON 01 NOV 2002

FILE 'CAPLUS' ENTERED AT 16:57:44 ON 01 NOV 2002
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=> d hist

     (FILE 'HOME' ENTERED AT 16:08:21 ON 01 NOV 2002)

     FILE 'REGISTRY' ENTERED AT 16:09:02 ON 01 NOV 2002
L1           61 S GARGARGGNACNGCNGTNCC/SQSN
L2            6 S GARTTYCARAARGAYATHGAYMG/SQSN
L3            3 S TTYGTNAAYGTNATHTGYGGNGC/SQSN
L4              QUE TGNCKDATNSWYTCRTCRAAYTC/SQSN
L5              QUE TGNCKRTCYTTRTANGCRTCYTG/SQSN
L6              QUE GGNGCRAADATNCKYTGNCKRTC/SQSN
L7            3 S L4
L8            3 S L5
L9            3 S L6

     FILE 'BIOSIS, MEDLINE, CAPLUS, EMBASE' ENTERED AT 16:57:44 ON 01 NOV 2002

=> s l1 and l2 and l3 and l7 and l8 and l9
L10           1 L1 AND L2 AND L3 AND L7 AND L8 AND L9

=> s l1 or l2 or l3 or l7 or l8 or l9
   3 FILES SEARCHED...
L11          11 L1 OR L2 OR L3 OR L7 OR L8 OR L9

=> d l10 pn py ab ti so au

L10  ANSWER 1 OF 1  CAPLUS  COPYRIGHT 2002 ACS
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09921880

	PATENT NO.	KIND	DATE
PI	WO 2001021657	A1	20010329
	EP 1132400	A1	20010912

PY 2001
2001

AB A novel antibacterial protein whereby the growth of plant pathogenic bacteria, for example, Pyricularia oryzae and Rhizoctonia solani, which are causative of the two major diseases of rice, can be inhibited at a relatively low concn., cDNA, and recombinant expression, are disclosed. A method of isolating the protein from Lyophyllum shimeji with ammonium sulfate pptn., and ion-exchange chromatog., are claimed. Antibacterial agents contg. the protein are claimed. The antibacterial protein isolated from Lyophyllum shimeji had a mol. wt. of 70 kDa and about 65 kDa when detd. by the SDS-PAGE method. The protein both isolated and recombinantly expressed in E. coli showed pyranose oxidase activity toward glucose and 1,5-anhydroglucitol.

TI Lyophyllum shimeji antibacterial protein with pyranose oxidase activity

SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2

IN Takakura, Yoshimitsu; Kuwata, Shigeru; Inoue, Yasuhiro

=> s l11 not l10
L12 10 L11 NOT L10

=> dup rem
ENTER L# LIST OR (END):l12
PROCESSING COMPLETED FOR L12
L13 9 DUP REM L12 (1 DUPLICATE REMOVED)

=> s l13 and py<=1999
1 FILES SEARCHED...
L14 4 L13 AND PY<=1999

=> d 1-4 l14 py pn au ti so ab

L14 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
PY 1994
AU Bilsland, Caroline A. G.; Springer, Timothy A. (1)
TI Cloning and expression of the chicken CD18 cDNA.
SO Journal of Leukocyte Biology, (1994) Vol. 55, No. 4, pp. 501-506.
ISSN: 0741-5400.
AB The leukocyte integrins play a critical role in a number of cellular adhesive interactions during the immune response. We describe here the isolation and characterization of the chicken beta-2 (CD18) subunit, common to the leukocyte integrin family. The deduced 748-amino acid sequence reveals a transmembrane protein with 65% and 64% identity with its human and murine homologues, respectively. The chicken beta-2 can associate on the cell surface with the human alpha subunit of LFA-1 and yields a hybrid molecule capable of binding to purified ICAM-1 and ICAM-3.

L14 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2002 ACS
PY **1999**
AU Dunham, I.; Shimizu, N.; Roe, B. A.; Chissoe, S.; Dunhyam, I.; Hunt, A. R.; Collins, J. E.; Bruskiewich, R.; Beare, D. M.; Clamp, M.; Smink, L. J.; Alnscough, R.; Almeida, J. P.; Babbage, A.; Bagguley, C.; Balley, J.; Barlow, K.; Bates, K. N.; Beasley, O.; Bird, C. P.; Blakey, S.; Bridgeman, A. M.; Buck, D.; Burgess, J.; Burrill, W. D.; Burton, J.; Carder, C.; Carter, N. P.; Chen, Y.; Clark, G.; Clegg, S. M.; Cobley, V.; Cole, C. G.;

Collier, R. E.; Connor, R. E.; Conroy, D.; Corby, N.; Coville, G. J.; Cox, A. V.; Davis, J.; Dawson, E.; Dhaml, P. D.; Dockree, C.; Dodsworth, S. J.; Durbin, R. M.; Ellington, A.; Evans, K. L.; Fey, J. M.; Fleming, K.; French, L.; Garner, A. A.; Gilbert, J. G. R.; Goward, M. E.; Grafham, D.; Griffiths, M. N.; Hall, C.; Hall, R.; Hall-Tamlyn, G.; Heathcott, R. W.; Ho, S.; Holmes, S.; Hunt, S. E.; Jones, M. C.; Kershaw, J.; Kimberley, A.; King, A.; Laird, G. K.; Langford, C. F.; et al.

TI The DNA sequence of human chromosome 22

SO Nature (London) (**1999**), 402(6761), 489-495
CODEN: NATUAS; ISSN: 0028-0836

AB Knowledge of the complete genomic DNA sequence of an organism allows a systematic approach to defining its genetic components. The genomic sequence provides access to the complete structures of all genes, including those without known function, their control elements, and, by inference, the proteins they encode, as well as all other biol. important sequences. Furthermore, the sequence is a rich and permanent source of information for the design of further biol. studies of the organism and for the study of evolution through cross-species sequence comparison. Here, the sequence of the euchromatic part of human chromosome 22 is presented. The sequence obtained consists of 12 contiguous segments spanning 33.4 megabases, contains at least 545 genes and 134 pseudogenes, and provides the first view of the complex chromosomal landscapes that will be found in the rest of the genome.

L14 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2002 ACS

PY **1995**

AU Courty, Yves; Rosinski-Chupin, Isabelle; Rougeon, Francois

TI Various transcripts are generated from the VCSA1 gene by alternative splicing and poly(A) processing in the rat submandibular gland

SO Gene (**1995**), 162(2), 291-6
CODEN: GENED6; ISSN: 0378-1119

AB The members of the VCS (variable coding sequence) multigene family display extensive evolutionary divergence in the protein-coding region. The first described gene (VCSA1) was found to encode a major 0.7-kb mRNA (VCSA1*1T1) coding for a prohormone-like preproprotein, SMR1-VA1, in the submandibular gland (SMG) of Rattus norvegicus. The authors report here the cloning of four other VCSA1 cDNAs corresponding to mRNAs (VCSA1*1T2 to *1T5) expressed in the SMG. VCSA1*1T1 to *1T4 mRNAs share the three exons previously described and differ in their 3' untranslated regions (UTR). Their differences originate from the alternative utilization of four polyadenylation sites. Comparison of the tissue levels of VCSA1*1T1 and VCSA1*1T4 during post-natal development of the male rat SMG suggests that the poly(A) addn. sites are both used at each stage. The fifth RNA transcript (VCSA1*1T5) contains only the first two exons. The nucleotide sequence of the cDNA reveals that VCSA1 has an addnl. exon (exon 4) which is spliced to exon 2 in VCSA1*1T5. In addn. to VCSA1*1T1, at least VCSA1*1T4 and VCSA1*1T5 are actively translated in vivo, as revealed by their assocn. to the polysomal fractions. The protein, P2-VA1, coded by VCSA1*1T5 is 68 amino acids in length and it is likely to be a glycosylated secretory protein. The putative mature P2-VA1 protein completely differs from the SMR1-VA1 pro-protein and very likely has a different function. VCSA1*1T1 is accumulated in the male rat SMG 200-1000-fold more than the other transcripts. Run-on expts. reveal that almost all transcription proceeds several hundred bp downstream from the poly(A) site corresponding to VCSA1*1T1. This suggests that the high levels of VCSA1*1T1 transcript are mainly due to post-transcriptional events.

L14 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2002 ACS

PY **1990**

09921880

AU Rosinski-Chupin, Isabelle; Rougeon, Francois
TI The gene encoding SMR1, a precursor-like polypeptide of the male rat submaxillary gland, has the same organization as the preprothyrotropin-releasing hormone gene
SO DNA and Cell Biology (**1990**), 9(8), 553-9
CODEN: DCEBE8; ISSN: 1044-5498
AB SMR1 is a precursor-like polypeptide of the submaxillary glands of rats. Sequence anal. predict that it could be processed by maturation enzymes to release a small peptide resembling the TSH-releasing hormone. The SMRL1 gene was isolated from a rat genomic library and sequenced. The SMR1 gene spans 4.7 kb and consists of 3 exons. The 2 introns occur a few nucleotides before the initiation codon in the 5' untranslated region, and a few nucleotides before the first predicted processing site, resp. Such a structure is reminiscent of that of the preprothyrotropin-releasing hormone gene. The site of transcriptional initiation of the SMR1 gene was detd. and 1.4 kb of 5'-flanking sequence was sequenced. The sequence anal. revealed the presence of alternating purine-pyrimidine tracts and of purine-rich sequences. In addn., some sequences which could be involved in the regulation of SMR1 gene expression were identified.

=> d hist

(FILE 'HOME' ENTERED AT 16:08:21 ON 01 NOV 2002)

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L1 61 S GARGARGGNACNGCNGTNCC/SQSN
L2 6 S GARTTYCARAARGAYATHGAYMG/SQSN
L3 3 S TTYGTNAAYGTNATHTGYGGNGC/SQSN
L4 QUE TGNCKDATNSWYTCRTCRAAYTC/SQSN
L5 QUE TGNCKRTCYTTRTANGCRTCYTG/SQSN
L6 QUE GGNGCRAADATNCKYTGNCKRTC/SQSN
L7 3 S L4
L8 3 S L5
L9 3 S L6

FILE 'BIOSIS, MEDLINE, CAPLUS, EMBASE' ENTERED AT 16:57:44 ON 01 NOV 2002
L10 1 S L1 AND L2 AND L3 AND L7 AND L8 AND L9
L11 11 S L1 OR L2 OR L3 OR L7 OR L8 OR L9
L12 10 S L11 NOT L10
L13 9 DUP REM L12 (1 DUPLICATE REMOVED)
L14 4 S L13 AND PY<=1999

=> s l13 and pyranose
L15 0 L13 AND PYRANOSE

=> s l13 and antimicrobial
L16 0 L13 AND ANTIMICROBIAL

=> s l13 and (· Antimicrobial or bactericidal or fungicidal or microbicidal or antibacterial or anti-bacterial or antifungal or anti-fungal or bactericide or fungicide)
L17 0 L13 AND (7 ANTIMICROBIAL OR BACTERICIDAL OR FUNGICIDAL OR MICROB ICIDAL OR ANTIBACTERIAL OR ANTI-BACTERIAL OR ANTIFUNGAL OR ANTI-FUNGAL OR BACTERICIDE OR FUNGICIDE)

=> s l13 and (Antimicrobial or bactericidal or fungicidal or microbicidal or antibacterial or anti-bacterial or antifungal or anti-fungal or bactericide or fungicide)
L18 0 L13 AND (ANTIMICROBIAL OR BACTERICIDAL OR FUNGICIDAL OR MICROBIC IDAL OR ANTIBACTERIAL OR ANTI-BACTERIAL OR ANTIFUNGAL OR ANTI-FU NGAL OR BACTERICIDE OR FUNGICIDE)